

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/517,324B
Source: FWO
Date Processed by STIC: 7/6/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/5/97, 324B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 ✓ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/517,324B

DATE: 07/06/2006

TIME: 18:15:02

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\07062006\J517324B.raw

*See item 4 on Error
Summary sheet*

3 <110> APPLICANT: SinoGenoMax Company Ltd
W--> 4 <120> TITLE OF INVENTION: Randomised DNA libraries and double-stranded RNA libraries,
use and
W--> 5 method of production thereof
7 <130> FILE REFERENCE: P06031PC00
W--> 8 ~~<140>~~ CURRENT APPLICATION NUMBER: PCT/SE2003/001077B
C--> 9 ~~<141>~~ CURRENT FILING DATE: 2004-12-20
10 <150> PRIOR APPLICATION NUMBER: US 60/390,108
11 <151> PRIOR FILING DATE: 2002-06-21
W--> 12 <160> NUMBER OF SEQ ID: 45
13 <170> SOFTWARE: PatentIn version 3.1

change to

> <1507

> <1517

*There are
prior data.*

see pp 1, 4-5

ERRORED SEQUENCES

168 <210> SEQ ID NO: 15
169 <211> LENGTH: 19
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
W--> 172 <220> FEATURE:
173 <223> OTHER INFORMATION: 19 base pair clone

W--> 174 <400> SEQUENCE: 15
E--> 174 *where are nucleotides?*

321 <210> SEQ ID NO: 31
322 <211> LENGTH: 9
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence

W--> 325 <220> FEATURE:
326 <223> OTHER INFORMATION: primer

W--> 327 <400> SEQUENCE: 31

328 ttcaagaga

E--> 329 *this goes at beginning of sequence 32 in <2107*

348 <210> SEQ ID NO: 34 *This needs explanation*

349 <211> LENGTH: 19

350 <212> TYPE: DNA

351 <213> ORGANISM: Artificial Sequence

352 <221> NAME/KEY: misc_feature

353 <222> LOCATION: (1)...(19)

W--> 354 <220> FEATURE:

354 <223> OTHER INFORMATION: n= a, "t", "c", or "g"

E--> 355 <400> SEQUENCE: 34

W--> 356 nnnnnnnnnnnn nnnnnnnnnn

**Does Not Comply
Corrected Diskette Needed**

*insufficient explanation - give source of
genetic
material*

*(see item 11 on
Error Summary
sheet)*

9

*Insert <2207 wherever <2217, <2227,
or <2237
is shown*

<2207

19

VERIFICATION SUMMARY

DATE: 07/06/2006

PATENT APPLICATION: US/10/517,324B

TIME: 18:15:03

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\07062006\J517324B.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
 L:8 M:283 W: Missing Blank Line separator, <140> field identifier
 L:8 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:12 M:283 W: Missing Blank Line separator, <160> field identifier
 L:19 M:283 W: Missing Blank Line separator, <220> field identifier
 L:21 M:283 W: Missing Blank Line separator, <400> field identifier
 L:28 M:283 W: Missing Blank Line separator, <220> field identifier
 L:30 M:283 W: Missing Blank Line separator, <400> field identifier
 L:37 M:283 W: Missing Blank Line separator, <220> field identifier
 L:38 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
 L:41 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
 L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
 L:44 M:283 W: Missing Blank Line separator, <400> field identifier
 L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
 L:67 M:283 W: Missing Blank Line separator, <220> field identifier
 L:69 M:283 W: Missing Blank Line separator, <400> field identifier
 L:76 M:283 W: Missing Blank Line separator, <220> field identifier
 L:78 M:283 W: Missing Blank Line separator, <400> field identifier
 L:85 M:283 W: Missing Blank Line separator, <220> field identifier
 L:87 M:283 W: Missing Blank Line separator, <400> field identifier
 L:94 M:283 W: Missing Blank Line separator, <220> field identifier
 L:96 M:283 W: Missing Blank Line separator, <400> field identifier
 L:103 M:283 W: Missing Blank Line separator, <220> field identifier
 L:104 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
 L:107 M:283 W: Missing Blank Line separator, <400> field identifier
 L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
 L:114 M:283 W: Missing Blank Line separator, <220> field identifier
 L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
 L:118 M:283 W: Missing Blank Line separator, <400> field identifier
 L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
 L:125 M:283 W: Missing Blank Line separator, <220> field identifier
 L:126 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
 L:129 M:283 W: Missing Blank Line separator, <400> field identifier
 L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
 L:136 M:283 W: Missing Blank Line separator, <220> field identifier
 L:138 M:283 W: Missing Blank Line separator, <400> field identifier
 L:145 M:283 W: Missing Blank Line separator, <220> field identifier
 L:147 M:283 W: Missing Blank Line separator, <400> field identifier
 L:154 M:283 W: Missing Blank Line separator, <220> field identifier
 L:156 M:283 W: Missing Blank Line separator, <400> field identifier
 L:163 M:283 W: Missing Blank Line separator, <220> field identifier
 L:165 M:283 W: Missing Blank Line separator, <400> field identifier
 L:172 M:283 W: Missing Blank Line separator, <220> field identifier
 L:174 M:283 W: Missing Blank Line separator, <400> field identifier
 L:174 M:301 E: (44) No Sequence Data was Shown, SEQ ID:15
 L:174 M:252 E: No. of Seq. differs, <211> LENGTH:Input:19 Found:0 SEQ:15
 L:180 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

DATE: 07/06/2006

PATENT APPLICATION: US/10/517,324B

TIME: 18:15:03

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\07062006\J517324B.raw

L:182 M:283 W: Missing Blank Line separator, <400> field identifier
L:189 M:283 W: Missing Blank Line separator, <220> field identifier
L:191 M:283 W: Missing Blank Line separator, <400> field identifier
L:198 M:283 W: Missing Blank Line separator, <220> field identifier
L:200 M:283 W: Missing Blank Line separator, <400> field identifier
L:207 M:283 W: Missing Blank Line separator, <220> field identifier
L:209 M:283 W: Missing Blank Line separator, <400> field identifier
L:216 M:283 W: Missing Blank Line separator, <220> field identifier
L:218 M:283 W: Missing Blank Line separator, <400> field identifier
L:225 M:283 W: Missing Blank Line separator, <220> field identifier
L:227 M:283 W: Missing Blank Line separator, <400> field identifier
L:234 M:283 W: Missing Blank Line separator, <220> field identifier
L:236 M:283 W: Missing Blank Line separator, <400> field identifier
L:243 M:283 W: Missing Blank Line separator, <220> field identifier
L:245 M:283 W: Missing Blank Line separator, <400> field identifier
L:252 M:283 W: Missing Blank Line separator, <220> field identifier
L:253 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:329 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:10 SEQ:31
L:329 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:329 M:252 E: No. of Seq. differs, <211> LENGTH:Input:9 Found:10 SEQ:31
L:354 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:355 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:34
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:390 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:454 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0

10/517,324B

4

<210> 3
<211> 500
<212> DNA
<213> Artificial Sequence
<220>
<221> misc-feature
<222> (7)... (7)
<223>n=a, "t", "c", or "g"
<221> misc-feature
<222> (9)... (9)
<223>n=a, "t", "c", or "g"
<400> 3

this needs explanation in 'C2207-C2237
section'. see item 11 on Error Summary
sheet.

same error in seqs. 8-10, 24, 25,
26, 34, 38, 39, 42, 43, 44, 45

<210> 27
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <222> (17)... (35)
 <223> RNA coding sequence
 <400> 27

ggggaagatc taaaaaata aatgaatcaa gaacattttt aagcttgggg

PyD: This is an insufficient
 explanation for <213> Artificial Sequence

what about locations 1-16, 36-50?

They need explaining,

50 since the

<213>

response

"Artificial Sequence"

same error in seq. 28-30

give source of genetic
material

as explanation